

Fig. 1

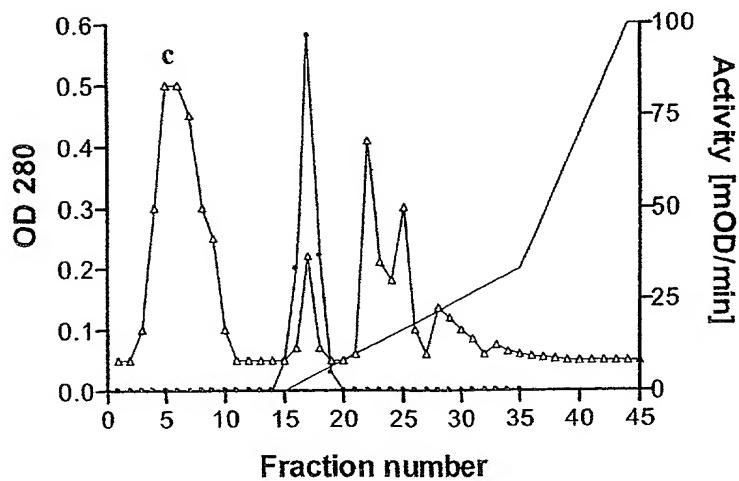
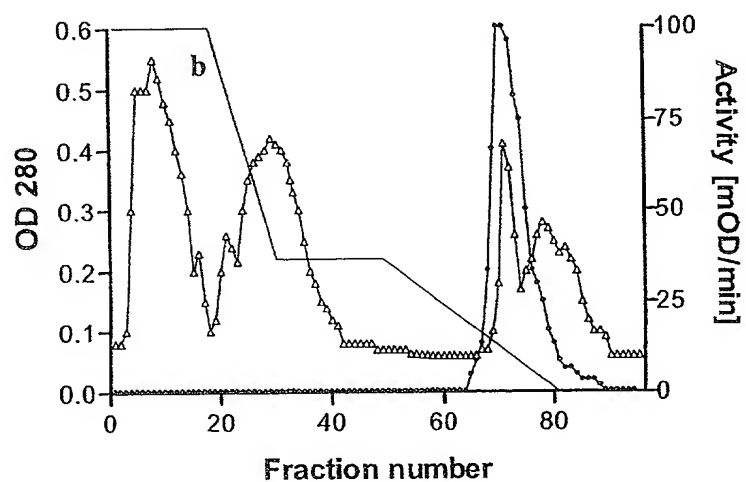
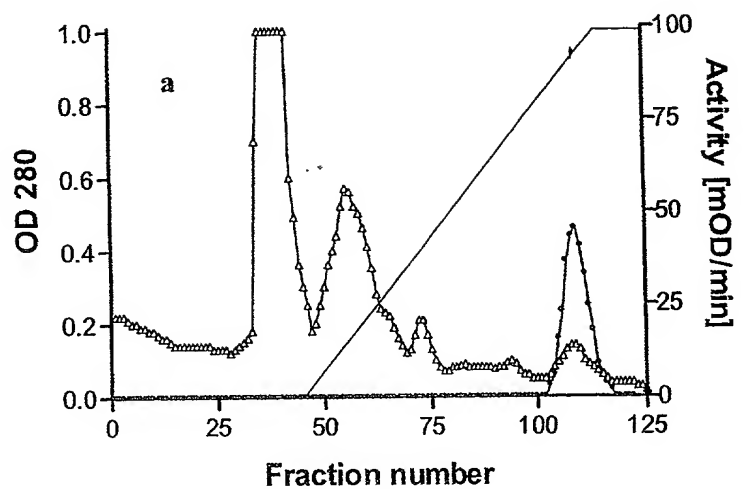


Fig. 2

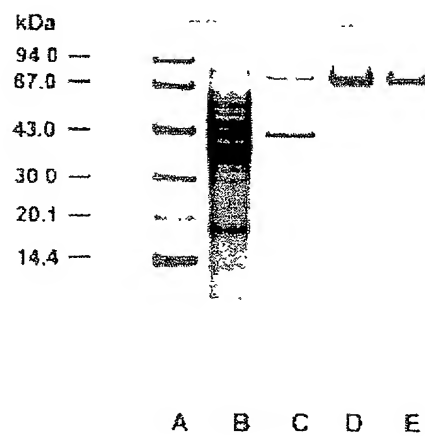
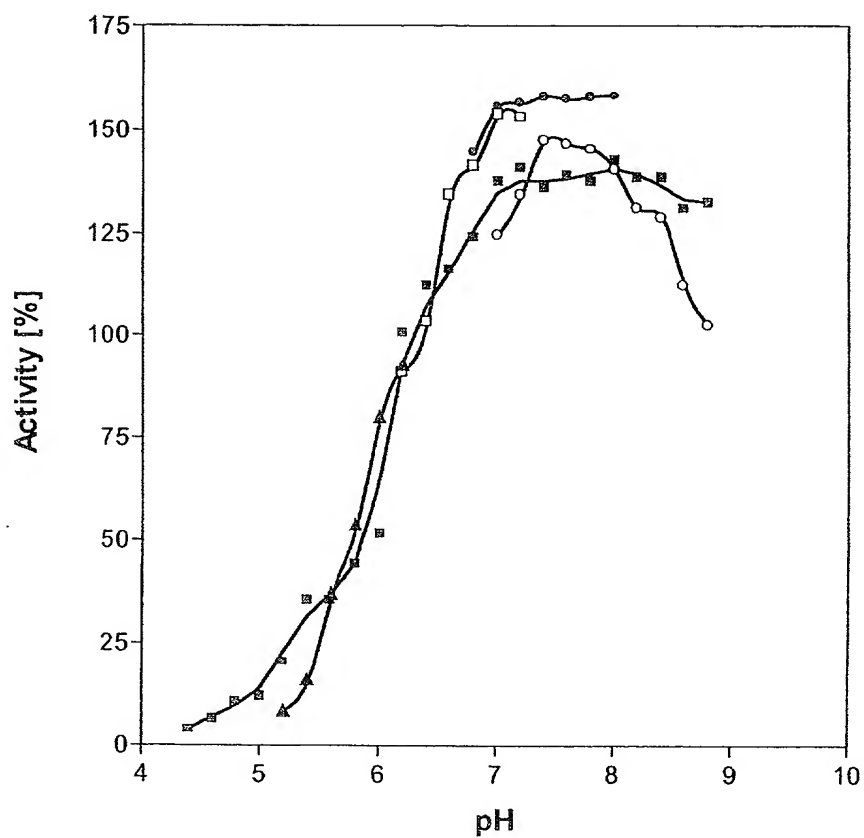


Fig. 3



SQR ID NO: 1  
SQR ID NO: 2

[illegible]

TDEDT "SSESDDT

Fig. 5

Seq ID No: 3 DPP-7	644	TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFFDLQRTISVDIRYVLFM	695
		TGGNSGSPVF++ +IG+ + G +G +	+I + F
Seq ID No: 4 V-8	704	TGGNSGSPVFNEKNEVIGIHWGVPNEFNGAVFINENVRNFKQNTIEDIHFA	863

Fig. 6

SEQ ID NO: 5 S1 1 MASQALGFLHONGINTMKWLLSVAVAAAFASHADECMWPHOLP-AMADVLAKKLEHDAKSKLTFEPN--AVHSL  
 S2 1 -----MRJIAVAAVLTCTGATADEGQWQYQMP-SHADKLSAGCHDPAKADLATSYPMN--AVVGL  
 SEQ ID NO: 6 X 1 -----MRFNLSLSVLAHLITVDSTHAGECMWVPOOLP-EHAGPLKQAGLO-SPEQSNLIGDEM--AVVSL  
 SEQ ID NO: 7 P1 1 -----MQMKLSIHLGAALHILGASGVAKADKGMWFLNEINQENLDRMELGFTPLD-SYSDKPSHANAVVHFG  
 P2 1 -----MKRHLPLFVAVLCLCQIAHADEGMWLMQOLG-RKYAQKREKGLKKEYDYFNPNGTSTKDAVVIFD  
 SEQ ID NO: 8 S1 78 GGCTASFVSPKGLVWNNHHCAYGSIQVNSTPEKNLLODGFIAKTFADLPAAPGSRVVTEDYTNVIERVKAQENKGTG--  
 S2 62 CYCTASFVSPKGLVWNNHHCAYKAIQYNKKEHNYLECGFIATSDKXEPSAGNEPRLVTEAVTDTSDTKDLSDP--  
 X 66 CUNCTASIVSPEGLVITNNHHCAYGAIQNSTPKKNLKEGENALTOADEVSGAGNARHYVEQLTDTVTAQAKALAAAGND  
 P1 71 GGCTGITVSDQGLHFTNNHHCYGAIQOSQSTVDHDLRDCGFVSRMCG-BELPIGCLSVKVPKIVKVTDKVCEQKGITD-  
 P2 67 GGCTGEVVSDDRGLVITNNHHCYDMQIAHSTLEHNYLENGEFWAMREA-DELPNKDISVVEHKLLEDTVTVKKDKKAIKDP  
 S1 157 -----REFYQGVNQEKALVAECEKDEGYRCQVYSEHGGLEYHMLKOLEITDVLRLVYNPACSVGKGGVDNNMWPRHT  
 S2 140 -----LKRYEEIENHSHKALIKSCAADNRYCAVRSEHNGLEFVMILOIMIEDVRLVYADPE-SVCGGGIDNNTYPRHS  
 X 146 -----PEKRTTALLETFSKOEIAKCEEEOGYRCQVYSEHNGLEFVMILOIMIEDVRLVYADPE-SVCGGGIDNNTYPRHS  
 P1 149 -----EMERLRKAQEVCOELAKKENADENQOLCIVEPEYSNNEHMLIYVDVVKDVRVYADPE-SVCGKFGCDTNNMWPRHT  
 P2 146 NSMDYLSPKYLQKLADKKAGKFNFAKNPCLSVETKAEHYGGNMLMFTKKTYTVDRLVYADPE-SVCGKFGCDTNNMWPRHT  
 S1 231 GDSFYRAYVSKNGKPAEFSAIDNMPYEPKRSFLKVSAGVSECGEVMVAGYPCPTNNRVTATERNVQNEFEWATYEGKMER  
 S2 214 GDFAFIRAYVGKDGKPAEFSEDNIPYTPKSLKKNADGVKAGCGVEVAGYPCPTNNRNLTSFKFASDMLYFTQAKRYOL  
 X 221 GDFSFRAYVGKDGKPAEFSEKNIPYTPKSLKKNADGVKAGCGVEVAGYPCPTNNRNLTSFKFASDMLYFTQAKRYOL  
 P1 224 GDFSFRAYVGKDGKPAEFSEKNIPYTPKSLKKNADGVKAGCGVEVAGYPCPTNNRNLTSFKFASDMLYFTQAKRYOL  
 P2 226 GDFSFRAYVGKDGKPAEFSEKNIPYTPKSLKKNADGVKAGCGVEVAGYPCPTNNRNLTSFKFASDMLYFTQAKRYOL  
 S1 311 FIEHIIKATAPEGSDERIKVESQIAGLANYAKNFTSMIEFYGKSTMLADEKALEAKAEWIAKDS--REAKYKTLAET  
 S2 294 QIDTIEAMGQKQDADIAIKYAGNMASMANRMKLNGLHAGKATDVGITKQORENDFHAWTKNPN-----LNQNLISEL  
 X 301 LIATIEAASKQNPDIQKYASTLAGNNTSKNFTCQDGHRIINAQKQSEETATIAWIKQOCI--RGHEALAAHQTIL  
 P1 304 KQGIWKEAMSADQATRIKIVASKYAQSANYWKNSTIGNRLGLARDYIGRKAEEERAFADWIRKNGKSAV---YGDVLSLE  
 P2 306 RQGVILREMLADPOIKIMYSAKYAASQAYKRAICANWALITRGIRONKQAMQDRWANGAKQCTP-----RYEEAVHE  
 S1 388 DALIAKSKAQERDMITSYISSTVPTANNILYRLAHEKQLEDMQREPCQDRDVTFRFKASVERIDRRYAAASVDKAVLFD  
 S2 368 EVLLAEQOLOTNVTYFTNAQSSITPTANNILYRLAHEKQLEDMQREPCQDRDVTFRFKASVERIDRRYAAASVDKAVLFD  
 X 378 VDLTEQYKANQDRDEVTGQNGSGVIGVAVNLYRLAIEETKSDAQREACQOERDLEPTIEGNLKQERRYLPEMDROMQOY  
 P1 381 KAYKEGAKANREMTYLSITLFGGEVVRFAAFANALATNPDAHAGILKSLDDKYDYLPISLDRKVLPAMLDIVRRTPAD  
 P2 380 IDATVAKRADLRRLMYIEEGIRGEIEFARSPITPTEDETKALQONDASRKEAIDKIRTRYSKFANKOYSAEVDKKAYVA  
 S1 468 MKRYAALPEAQRIEPAQKAFEDNKNVNEAKLAKTIDKMYAKTEICGNKQVRLAWMEKSVDDDEKASKDPTIQEAVAMMDTN  
 S2 448 DEN--AYLSQPNRVAALDNNMLNDKN--VSLAAKIDGLYSITLITDQAQRIAWMEADAKALETSSDPEIRLAVALYDIN

X 458 WITEYKLPVKORVAMDVWIGDGIPAT-----L-KRLGDKLSSSEERLKMENADRAABESSQDPAIRMAVAIMPAL  
P1 461 KLPDLFKNVIDKKFKGDTKKYADFVD--KS-----VVPYSDFHAKSMDEKKEKAIEKDPAVELSKSVIAAA  
P2 460 MITEYLKEIPYENPLHLRLVKORFAG-----DVQAYVDDIFARSVFGSEAOFDFAFAVPSVEKLAEDENAVLEASSVEDEY  
  
S1 548 MSEEKKEKELDCEIMKVRPOYMDAIRIAYNLEQCKPVYADANSSLRVTCHVKGYSPKDCIVAVPFTTRLEGIVOKDTG--ID  
S2 524 AOERAEKILACKLSTARPAMAAVYDYKANNWPVYPDANGTLRLSYGWDGYQSRDATTKOPFTRLDGLVAKHTG--YE  
X 530 EIERONKIRTCEILKARPITYLOALADYNKSHGKVYPDANSIARITTECHVKGYSPKDCVETPFTTTIOGVAKNTG--YE  
P1 530 RAIQADAMANAYAIKGRLEFAGIREMYP--GRALPSDANFTMRMSYCSIKGYEPQDCAWNYHTTICKGVLEKQDPKSD  
P2 536 RKLYNELRPYDDPILRAQRTYIAGILEMDG--DQDQEPDANLTIRETYQVKGYSPRDNAYVCHQTTILDGVMEKEDPDNW  
  
S1 627 PEDAPKQOLEHIKQKQYGDYXMKSIDS-----VPVNFSLSTDTTTCGNSGSPTENGRAEIVGLLE  
S2 603 PYNAPKLLDAISVQREGDHLVKSVOYQDPRGWICRLFSCLDKPEEFNSVPVNFSSVDITTCGNSGSPVENGKGLVGLNE  
X 609 PEDSPKSLINAIKAKSYANLADQRIGT-----VPVNFSLSDITTCGNSGSPVLDHAKGLVGLAF  
P1 608 EFAVOENLIDIFRTKNYGRVAENGOLH-----TAF--LSNNDITTCGNSGSPVEDKNCPILIGLAF  
P2 614 EHVVDPKIKAVYERKDEGRVADRSGRMP-----VAFQATHTTTCGNSGSPVMNANGELIGINE  
  
S1 686 DGVYESHIGGMAEDNEINRSIHVDSTRYMLWMKVFDFHADNLLAEVEHYN-  
S2 683 DSTYEALTKOWFENPTITRAVHVDIRYLLWMDEVDHADNLIKEDDIFVRN-  
X 668 DGNWESVSNWVEDPVMTRITIAVDSTRYVQWIMTEVAPAPHLIKENIFYR-  
P1 665 DGNWEAMSGDIEFEEDLQRTISVDIRYVLFEMDKW-----  
P2 672 DRNWEVGGDIQYIADYORSIINDIRYVLFVIDKVGCCQRLDENNRP--